

Figure 1.

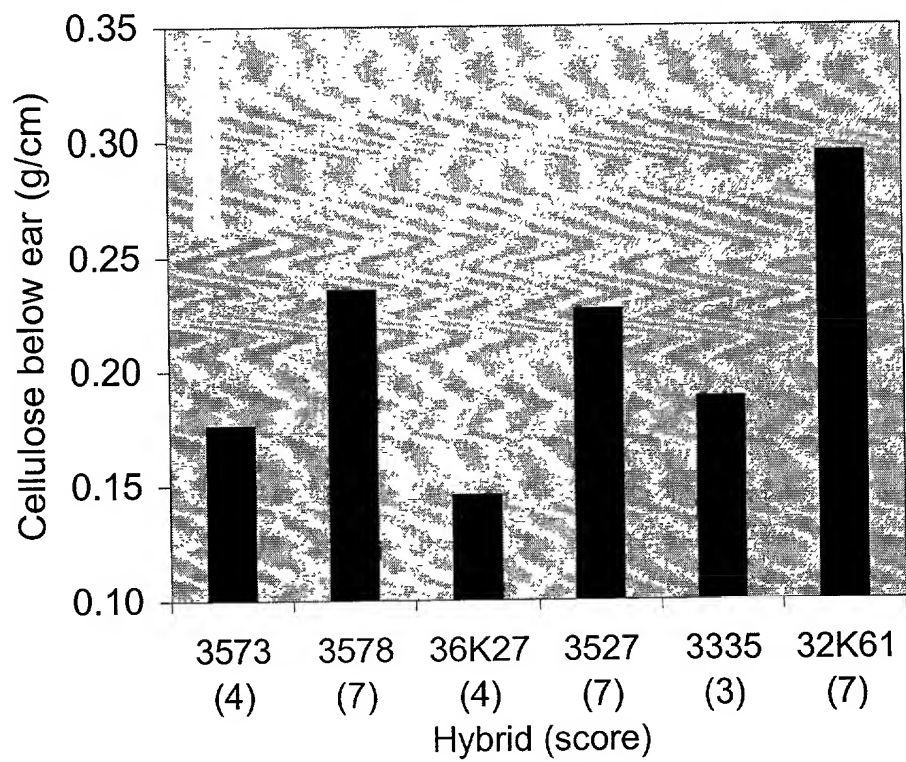


Figure 2

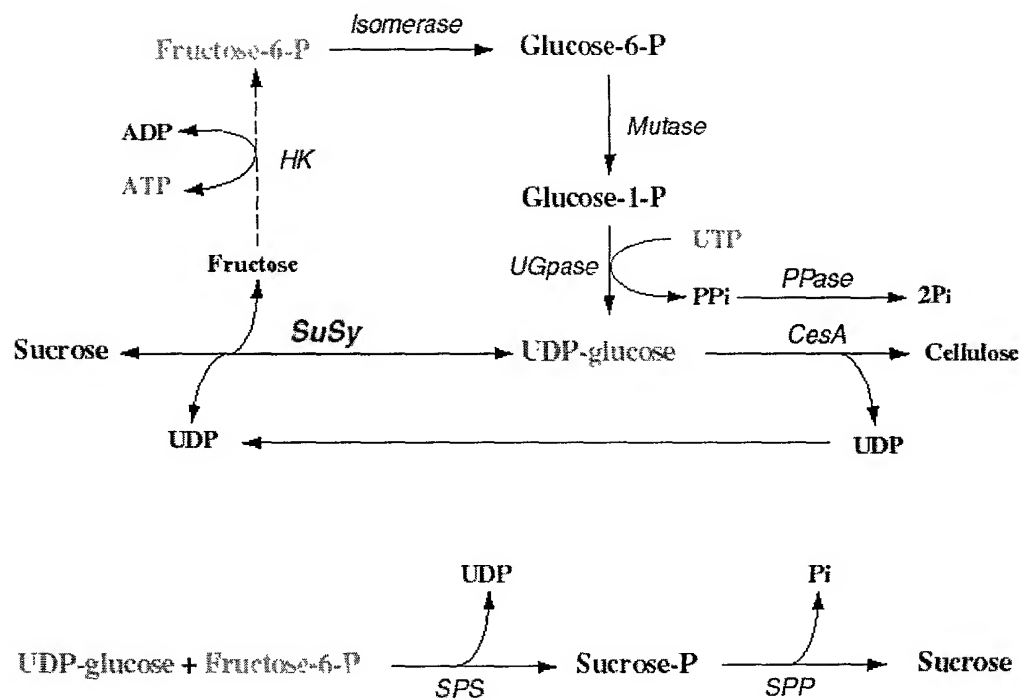


Figure 3.

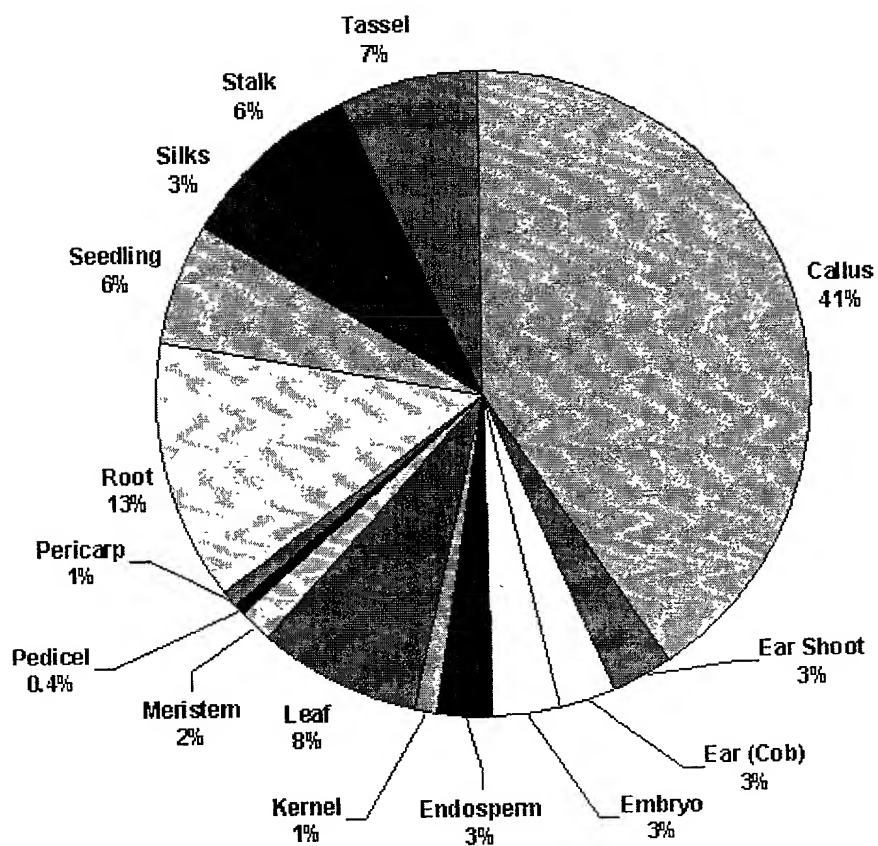


Figure 4.

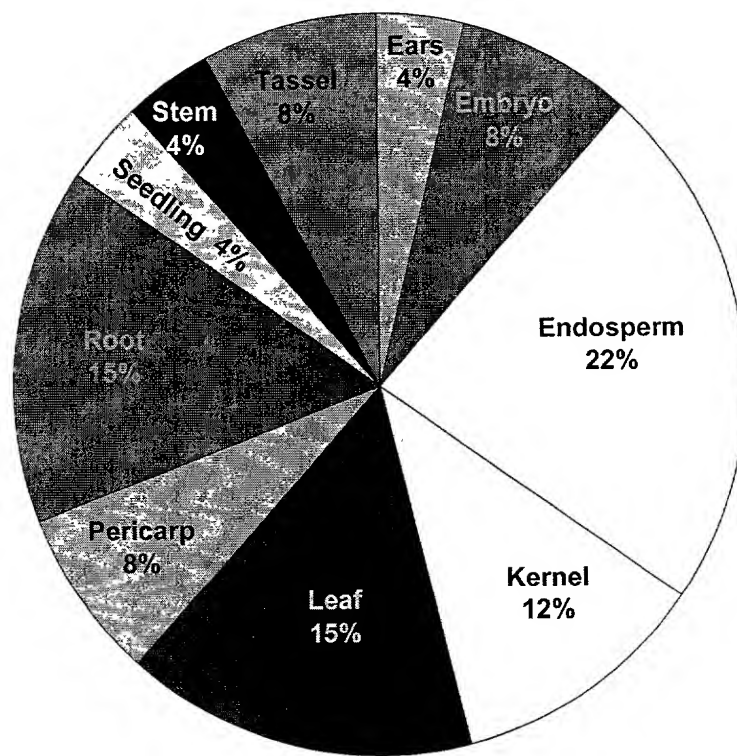


Figure 5

Allele 1: CACCCGG-mu-AGATTG

Allele 2: CACC-mu-CGGAGATTG



Figure 6.

Figure 7.

Genotype	structural dry matter (% of total dry matter)	cellulose (% of total dry matter)	cellulose (% of structural dry matter)
<i>Sus-1</i> (WT)	63.2	25.2 +/-0.38	39.9
<i>sus-1</i> (mutant)	47.3	17.7 +/-0.34	37.4

1008014.022402

		1	50
Sh1	(1)	-----MAAKLTRLSRLRERIGATFSSHPNELIALFSRYVHQCKGMLQPHQ	
Sus1	(1)	MGEAGDRVLSRLHSVRERIGDSLSAHPNELVAVFTRLKNLCKGMLQPHQ	
Sus3	(1)	-----STHASGDRVEDTLHAHRNEELVALLSKYVNKCKGILQPHH	
Consensus	(1)	LSRLHSRLRERIGDTLSAHPNELVALFSRYVN GKGMQLQPHQ	
		51	100
Sh1	(46)	LLAEFD-ALFDSDE--KYAPFEDILRAAQEAIVLPWVALAIRPRPGVW	
Sus1	(51)	ITAEYNNATPEAREKLKDGAFEDVLRAAQEAIVLPWVALAIRPRPGVW	
Sus3	(40)	ILDALDEVQSGGRA-LAEGPELQVLRSAQEAIVLPFVAIAVRPRPGVW	
Consensus	(51)	ILAEFD AI DADRE LKDGPFEDVLRAAQEAIVLPWVALAIRPRPGVW	
		101	150
Sh1	(93)	DYIRVNVSEMAVEELSVSEYLAPKEQLVDGQSNFVLELDFEPFNASFP	
Sus1	(101)	EYVRVNVSELAVEELRVPEYLQKEQLVREGPNNNFVLELDFEPFNASFP	
Sus3	(89)	EYVRVNVHLSVEQLTVSEYLRKEELVDGQHNDPVLVLELDFEPFNVSVP	
Consensus	(101)	EYVRVNVSELAVEELSVSEYL FKEQLVDGQ N NFVLELDFEPFNASFP	
		151	200
Sh1	(143)	RPSMSKSTGNGVQFLNRHLSSKLFQDKESLYPLLNFLKAHNYKGTMMLN	
Sus1	(151)	RPSLSKSTGNGVQFLNRHLSSKLFHDKESMYPLLNFLRAHNYKGMTMMLN	
Sus3	(139)	RPNRSSSTGNGVQFLNRHLSSIMERNRDCLEPLDPLRGHHRKHVMMLN	
Consensus	(151)	RPSLSKSTGNGVQFLNRHLSSKLF DKESLYPLLNFLRAHNYKG TMMLN	
		201	250
Sh1	(193)	DRIQSLRGLOSSIRKAEYLLSVPODTPYSEFNHRFOELGLEKGGWGTAK	
Sus1	(201)	DRIRLSALQCALRKAEHTISTLOADTPYSEFHHRFOELGLEKGGWGTAK	
Sus3	(189)	DRIQSLGRLOSVITKAEHTISKLPADTPYSOFAYKFOELGLEKGGWGTAK	
Consensus	(201)	DRIQSL ALQSAIRKAEHLSLPAADTPYSEF HRFQELGLEKGGWGTAK	
		251	300
Sh1	(243)	RVLDTLHLLELLEAPDPANLEKFLGTIPMMENVVILSPHGYFAQSNVLG	
Sus1	(251)	RAQETIHLLELLEAPDPSTLEKFLGTIPMVENVVILSPHGYFAQANVLG	
Sus3	(239)	HVLEMIHLLELDIQAPDPSTLEKFLGTIPMIFENVVILSPHGYFAQANVLG	
Consensus	(251)	RVLETIHLLELLEAPDPSTLEKFLGTIPMIFENVVILSPHGYFAQANVLG	
		301	350
Sh1	(293)	YPDTGGQVVYILDQVRALENEMLLRIKQOGLDITPKILIVRLLEDAAGT	
Sus1	(301)	YPDTGGQVVYILDQVRAMENEMLLRIKQOGLDITPKILIVRLLEDAAGT	
Sus3	(289)	LPDTGGQIVYILDQVRALENEMVLRKKOGLDVSPKILIVRLLEDAAGT	
Consensus	(301)	YPDTGGQVVYILDQVRALENEMLLRIKQOGLDITPKILIVTRLLPDA GT	
		351	400
Sh1	(343)	TCGQRLKVKVTEHTDLRVVPERNENGILRKWISRFDVWPYLETYTEDVS	
Sus1	(351)	TCGQRLKVKVTEHCHILRVVPERTENGIVRKWISRFVWPYLETYTDEVA	
Sus3	(339)	SCNQLERTSGTOHTYLLRVVPERNENGILKKWISRFDVWPYLETFAEDAA	
Consensus	(351)	TCGQRLKVKVTEHTHILRVVPERNENGILRKWISRFDVWPYLETYTEDVA	
		401	450
Sh1	(393)	SEIMKEMQAKPDLIIGNYSDGNLVATLAHLGVTOCTIAHALEKTKYPN	
Sus1	(401)	HEIAGELQANPDILIGNYSDGNLVACLLAHKMGVTHCTIAHALEKTKYPN	
Sus3	(389)	GEIAAELQGTDFIIGNYSDGNLVASLLSYKMGVOCNIAHALEKTKYPD	
Consensus	(401)	EIAAELQA PDLIIGNYSDGNLVASLLAHKMGVTOCTIAHALEKTKYPN	
		451	500
Sh1	(443)	SDIYLKEDSQYHESQFTADLIAMNHTDFIITSTFQEIAGSKDTVGOYE	
Sus1	(451)	SDIYWKKFEDHYHESQFTADLIAMNHADFIITSTFQEIAGSKDTVGOYE	
Sus3	(439)	SDIFWKNFDEKYHESQFTADLIAMNADFIITSTYQEIAGSKNTVGOYE	
Consensus	(451)	SDIYWKKFDD YHFSQFTADLIAMNHADFIITSTFQEIAGSKDTVGOYE	
		501	550
Sh1	(493)	SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSYFPHYTESKRLTSLH	
Sus1	(501)	SHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADLSYFPHYTESKRLTSLH	
Sus3	(489)	SHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSYFPHYTESKRLTSLH	
Consensus	(501)	SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSYFPHYTES KRLTSLH	

Figure 8a

		551		600
Sh1	(543)	PEIEELIYSDVENSEHKFVLKDKKKPTIESMARLDRVKNMGLVEMYGKN		
Sus1	(551)	PEIEELIYSOTENTSHKFVLNDRNKPTIFSMARLDRVKNITGLVBYGRN		
Sus3	(539)	GSIENLIYDPEONDEHIGHLDRSKPTILFSMARLDRVKNITGLVEAFKAC		
Consensus	(551)	PEIEELIYS ENSEHKFVL DR KPIIFSMARLDRVKNITGLVELYGKN		
		601		650
Sh1	(593)	ARLRRLANLVIVAGDHGK-ESKDREEQAEFKKMYSLIDEYKLGKHIRWTS		
Sus1	(601)	KRLQELVNLVVVCGDHGN-PSKDKEEQAEFKKMFDLIEQYNLNGHIRWTS		
Sus3	(589)	AKLRRLVNLVVVAGYNDVNKSKDREEIAEIEKMHEILKTHNLFQFRWIS		
Consensus	(601)	ARLRRLVNLVVVAGDHG SKDREEQAEFKKMHDLLID YNL GHIRWIS		
		651		700
Sh1	(642)	AQMNRVRNGELYRYICDTKGAFVOPAFYEAFGLTVIESMTGGLPTIATCH		
Sus1	(650)	AQMNRVRNGELYRYICDTKGAFVOPAFYEAFGLTVVEAMTCGLPTFATAY		
Sus3	(639)	AQINRAVNGELYRYIADTHGAFVOPALYEAFGLTVVEAMTCGLPTFATLH		
Consensus	(651)	AQMNRVRNGELYRYICDTKGAFVOPAFYEAFGLTVVEAMTCGLPTFAT H		
		701		750
Sh1	(692)	GGPAEITVDGVSGLHIDPYHSDKAADILVNFEKCKADESYWDEISQGGL		
Sus1	(700)	GGPAEITVHGVSGYHIDPYQGDKASALLVDFFDKQAE SHWSKISQGGL		
Sus3	(689)	GGPAEITEHCVSGFHIDPYHPEQAVNLMADEEDRCQODEDHVWNISGAGL		
Consensus	(701)	GGPAEIIHGVSGGFHIDPYH DKAALVDFFDKCKADPSHW ISQGGL		
		751		800
Sh1	(742)	QRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMFYALKYR		
Sus1	(750)	QRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMLYALKYR		
Sus3	(739)	QRIYEKYTWKLYSERLMTLAGVYGFWKYVSKLERLETRRYLEMFYILKFR		
Consensus	(751)	QRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMFYALKYR		
		801		817
Sh1	(792)	SLASQVPLSFD-----		
Sus1	(800)	IMASTVPLAVEGEPSSK		
Sus3	(789)	ELAKTVPLAID-QPQ--		
Consensus	(801)	SLASTVPLAID P		

Figure 8b



		1	50
Sh1	(1)	AAACCTCCCTCCCTCCCTCCATTGGACTGCTTGCTCCCTGTTGACCAATG	
Sus1	(1)	-----GCCTGAG-GATCCAGGAAGAGGACAG	
Sus3	(1)	-----	
Consensus	(1)	G CTG G TCC G GA A G	
		51	100
Sh1	(51)	GGTATTCTGAACCATCGAGCCATGGCTGCCAAGCTGACTCCCTTTCACAG	
Sus1	(26)	CA-ATGGGGGAAGGTGCAGGTACCGTGTCTCTGAGCCGCTCCACAG	
Sus3	(1)	-----CTCCGAC-CCACGC	
Consensus	(51)	AT G A T AG TG C CTGAGTCGCCTCCACAG	
		101	150
Sh1	(101)	TCTTCGGGAACCGCTTGGTGCCACCTTCTCCTCCCATCCCAATGAACCTGA	
Sus1	(72)	CGTCAGGGAGCGGATTTGGCGATCACTCTCTGCGCACCCCAATGAGCTTG	
Sus3	(13)	GTCCGGCGACCGCGTCCAGGACACCCCTCCACGCGCACCGCAACGAGCTCG	
Consensus	(101)	TC GCGA CGC TTGG GACACCCTCTCCGCCACCCCAATGAGCT G	
		151	200
Sh1	(151)	TAGCACTCTTTTCAGGTATGTTCAACAGGGCAAGGGAATGCTTCAGCGC	
Sus1	(122)	TCGCGCTCTTCACCAAGCTGAAAAACCTTGAAAGGGTATGCTGCAGCCC	
Sus3	(63)	TCGCGCTCTGTCCAAGTACGTGAACAAGGGGAAGGGCATCTGCAGCCG	
Consensus	(151)	TCGCGCTCTT TCCAGGTA GT AACCAGGG AAGGG ATGCTGCAGCCC	
		201	250
Sh1	(201)	CATCAGCTGCTTCGCGAGTTTGA---TGC---CCTGTT--TGATACTGA	
Sus1	(172)	CACCAGATCAATGCGGAGTAAACAATGCGATCCCTGAGCCTGAGCGCGA	
Sus3	(113)	CACCACATCTTCGACGCTTCGACGAGGT---CCAGGG-CTCCGGGGCC	
Consensus	(201)	CACCAGATCCTTGCGGAGTTTCGAC ATGC CCTG G CTGAG G GA	
		251	300
Sh1	(242)	CAAGGAGAAG--TATGCACCAATTGAAGACATTCCTCGTCTCCTCAGGA	
Sus1	(222)	GAAGCTCAG--GATCGTGCTTTGAGCATGTCCTGAGGGCAGCTCAGGA	
Sus3	(158)	CGCGCGTAGCCGAGGAGCCCTCCTCGACGTCTCTCCCTCCGCGCAGGA	
Consensus	(251)	CAAGC CAAG GATGGACC TTTGA GACGTCCT CG GC GCTCAGGA	
		301	350
Sh1	(290)	AGCAATTGCTGCTCCCCCATGGGTTCGACTTGCTATCAGGCCAAGGCCTG	
Sus1	(270)	GGCGATTCTCATCCCCCATGGGTTCGACTTGCCATCCGCGCTAGGGCTG	
Sus3	(208)	GGCGATTCTGCTGCGCGCTTCGTTGGCCATCGCGGTGCGCGCGCGCGG	
Consensus	(301)	GGCGATTGTGCTCCCCCATGGGTTCGACTTGC ATCCGCC AGGCCTG	
		351	400
Sh1	(340)	GTCTCTGGCATTACATTCGGGTGAATGTAAGTGAGCTGGCTGTGAGGAG	
Sus1	(320)	GTCTCTGGCATTACATTCGGGTGAATGTAAGTGAGCTGGCTGTGAGGAG	
Sus3	(258)	GAGTTTGGGAGTACCTCGCGGTCAACGTTACGAGCTCAGCCTCGAGCAG	
Consensus	(351)	GTGTCTGGGAGTACCT CGGGTCAACGT AGTGAGCTCGCTGT GAGGAG	
		401	450
Sh1	(390)	CTGAGTGTGTTTCTGAGTACTTGGCATTCAAGCAACAGCTGCTGGATGGACA	
Sus1	(370)	CTGAGACTTCTGAGTACCTGCAGTTCAAGCAACAGCTTGTGCAAGGAGG	
Sus3	(308)	CTCAGACTCTCGGACTACCTCCGCTTCAAGGAGGAGCTTGTGACCGCCA	
Consensus	(401)	CTGAGAGTTTCTGAGTACCTGC TTCAAGGAACAGCTTGTGGA GGACA	
		451	500
Sh1	(440)	ATCCAACAGCAACTTTGTGCTTGAAGTTGATTTTGAAGCCCTTCAATGCCT	
Sus1	(420)	CCCAACAACAACCTTTGTTCTTGAAGCTGGACTTTGAGCCATTCAATGCCT	
Sus3	(358)	GCACAATGATCCCTACCTTCTCGAGCTTGACTTCCAGCCGTTCAATGTCT	
Consensus	(451)	CCCAACAACAACCTTTGTTCTTGAAGCTTGACTTTGAGCC TTCAATGCCT	
		501	550
Sh1	(490)	CTTTCCTCGTCTTCCATGTGCAAGTCCATCGCAAAATGGAGTGAATTC	
Sus1	(470)	CCTTCCCCTGCTCTTCTGTTCAAAGTCCATTGGCAATGGCGTGCAGTTC	
Sus3	(408)	CAGTCCCACGCCCAAAATCCGTCATCATCTATTGCAAAACGGTGTGCAGTTC	
Consensus	(501)	CCTTCCC CGTCTTCTCTGTCAAAGTCCATTGGAAATGG GTGCAGTTC	

Figure 9a

		551	600
Sh1	(540)	CTTAACCGACACCTGTCGCTCCAAGTTGTTCCAGGACAAGGAGAGTTTCTA	
Sus1	(520)	CTCAACAGGCACCTGTCAATCAAAGCTCTTCCATGACAAGGAGAGCATGTA	
Sus3	(458)	CTCAACCGACACCTTGTCTCAATCATGTTCCGCAACAGGCATTGCTTGG	
Consensus	(551)	CTCAACCGACACCTGTC TCAAAG TGTTCCA GACAAGGAGAGCTTGT	
		601	650
Sh1	(590)	CCCCCTTGCTGAACTTCCTCAAGGCTCATAACTAGAAGCCGACGACGATGA	
Sus1	(570)	CCCCCTTGCTCAACTTCCTTCGCGCCGACAAGTACAAGGGGATCACCATGA	
Sus3	(508)	CCCCCTGCTTGGATTTCCTCCGTGCCACCGGCACAAGGGCATGTTATGA	
Consensus	(601)	CCCCCTTGCTGAACTTCCTCCG GCCACAAC TACAAGGGGA GAC ATGA	
		651	700
Sh1	(640)	TGTTGAATGACAGAATCCAAAGCCTTCGTGGTCTCCAATCATCCTTGAGA	
Sus1	(620)	TGTTGAACGACAGAATCCGCACTCTCACTGCTCTGCAAGGTGGCGTGAGG	
Sus3	(558)	TGCTTAATGATAGAATACAAAGCTTGGGGAGGCTTCACTCTGTGCTGACC	
Consensus	(651)	TGTTGAATGACAGAATCCAAAGCCT GTGGTCT CAATCTGCGCTGAG	
		701	750
Sh1	(690)	AAGGCAGAGGAGTATCTACTGAGTGTTCCTCAAGACACTCCCTACTCGGA	
Sus1	(670)	AAGCCTGAGGACCAACCTGTCCACCTACAAGCTGATACCCCATACTCTGA	
Sus3	(608)	AAAGCTGAGGACCACTTGTCAAGCTCCCTGCTGACACACCATACTGACA	
Consensus	(701)	AAGGCTGAGGAGCACCTGTC A CT CTTGCTGACAC CCATACTC GA	
		751	800
Sh1	(740)	GTTCAACCATAGGTTCCAAGAGCTTGGCTTGGAGAAGGTTGGGGTGACA	
Sus1	(720)	ATTTACCCACAGGTTCCAGGAACTTGGTCTGGAGAAGGTTGGCGTGATT	
Sus3	(658)	ATTTGCTTATAAAATTCAAGAGTGGGGCTGGAGAAAGCTTGGGGTGATA	
Consensus	(751)	ATTT ACCATAGGTTCCAAGAGCTTGGCCTGGAGAAGGTTGGGGTGATA	
		801	850
Sh1	(790)	CTGCGAAGCCTGTTCTCCACACACTCCACTTGCTTCTCGACCTCTTTGAG	
Sus1	(770)	GCGCTAAGCGTGACAGGAGACTATCCACCTCCTCTTGCACTCTCTGGAG	
Sus3	(708)	CAGCAGGACATGTTTGGAAATGATCCATCTCTCTTAGACATCATTCAG	
Consensus	(801)	C GC AAGCGTGTCTGGA AC ATCCACCTCCTTCT GACCTCCTTGAG	
		851	900
Sh1	(840)	CCCCCTGATCTGCGCAACTTGGAGAAGTTCCCTTGGAACTATAAGGAATGAT	
Sus1	(820)	CCCCCAGATCCGTCACCCCTGCAGAACTTCTTGGAAACGATCCCCATGCT	
Sus3	(758)	CCCCCAGACCCATATACCTTAGAGAAATTTCTTGGGAGGATCCCCATGAT	
Consensus	(851)	GCCCCAGATCC TCCACCCCTGGAGAAGTTCTTGGAAACGATCCCCATGAT	
		901	950
Sh1	(890)	GTTCAACGTTGTTATCTGTCTCTCATGGCTACTTGGCCAGTCAATG	
Sus1	(870)	GTTCAATGTCCTTATCCTCTCCCTCATGGTTACTTGGCTCAAGCTAATG	
Sus3	(808)	TTTAAAGTTCTTGTGCTATCCCCTCATGGATACTTTGGTCAAGCTAATG	
Consensus	(901)	GTTCAACGTTGTTATCCT TCCCCTCATGG TACTTCGCTCAAGCTAATG	
		951	1000
Sh1	(940)	TGCTTGGATACCTTCACATGGCGGTCAAGTTCTGTACATCTGGATCAA	
Sus1	(920)	TCTTGGGTTACCTTGACAACGGAGGCCAGGTTGTCTACATCTTGGATCAA	
Sus3	(858)	TATTAGGCTTGGCAGACACACAGGACAGATCGTCTATATACTGGACCAA	
Consensus	(951)	T TT GG TACCCTGACAC GGAGG CAGGTTGTCTACAT CTGGATCAA	
		1001	1050
Sh1	(990)	GTCCGTGCTTTGGAGAATGAGATGCTTCTGAGGATTAAGCAGCAAGGCCT	
Sus1	(970)	GTGGCGCTATGGAGAACGAAATGCTGCTGAGGATCAAGCAGTGTGCTCT	
Sus3	(908)	GTCCGTGCACTACAAATGAGATGCTTCTCCGTTTAAAGAAACAAGGGCT	
Consensus	(1001)	GTCCGTGCT TGGAGAATGAGATGCTTCTGAGGAT AAGCAGCAAG CT	
		1051	1100
Sh1	(1040)	TGATATCAC TCGAAGATCCTCATTTGTTACCAGGCTGTTGCCTGATGCTG	
Sus1	(1020)	TGATATCACGCGGAAGATCCTTATTGTCAAGAGGTTGCTCCCTGATGCAA	
Sus3	(958)	TGATGTTTCCCCAAGATTCTCATTTGTTACTCCGCTGATACCAGATGCAA	
Consensus	(1051)	TGATATCAC CCGAAGATCCTCATTTGTTACCAGGCTG T CTTGATGCAA	

Figure 9b

		1101		1150
Sh1	(1090)	CTGGCAGTACGTCCGGTCAGCCGCTGGAGAAGGTCATTGGTACTGAGCAG		
Sus1	(1070)	CTGGCACCAGCTGTGGCCAGCCGCTTGAGAAGGTCCTTGGCACCAGGAC		
Sus3	(1008)	AAGGAACATCATGCAATCAGCGGCTTGAGAGAACTAGTGAACACAGCAT		
Consensus	(1101)	CTGG AC AC TGCGGTCAAGCGCTTGAGAAGGTCATTGG AC GAGCAC		
		1151		1200
Sh1	(1140)	ACAGAGATCATTTCGGCTTCCTTCAGAAATGAGATGGCATCCTCCGCAA		
Sus1	(1120)	TGCCATATCCCTCGCGTGGCATTGAGAACAGAAACCGAATCGTTCGCAA		
Sus3	(1058)	ACTTACATATTACGAGTTCCTTCAGAAATGAAATGGGATACTTAAGAA		
Consensus	(1151)	AC ACATC TTCGCTTCCTTCAGAAATGAAATGG ATCCTTCGCAA		
		1201		1250
Sh1	(1190)	GTGGATCTCTCGTTTTCATGTCTGGCCATACCTGGAGACATACACTGAGG		
Sus1	(1170)	GTGGATCTCGCCATTTCAGTCTGGCCGTACCTGGAGACTTACACTGATG		
Sus3	(1108)	ATGGATATCAAGATTTCATGTCTGGCCATATCTGGAAACATTTCCTGAGG		
Consensus	(1201)	GTGGATCTC CGATTTCATGTCTGGCCATACCTGGAGACATACACTGAGG		
		1251		1300
Sh1	(1240)	ATGTTTCCAGTCAAATAATGAAAGAAATGCAGGCCAAGCCTGACCTTATC		
Sus1	(1220)	ACGTGGCGCATCAGATTGGCTGGAGAGCTTCAGGCCAATCCTGACCTGATC		
Sus3	(1158)	ATGCTGCTGCTCAAAATTCCTGCTCAATTACAAGGTATCCAGACTTCATA		
Consensus	(1251)	ATGTTGC GTGAAATTGCTG AGAA T CAGGCCAATCCTGACCT ATC		
		1301		1350
Sh1	(1290)	ATTGGCAACTACAGCGATGGCAACCTAGTCGGCACTCTGCTCGGCGCAAA		
Sus1	(1270)	ATCGCAAACTACAGTACCGAAACCTTGTTCGGTGTTCCTCGCCACAA		
Sus3	(1208)	ATTGCAAACTACACTGATGGAATCTTCTGGCGTCATTGGTATCTTACAA		
Consensus	(1301)	ATTGGAAACTACAGTATGGAACCTTGT GCGTCTTTGCTCGC CACAA		
		1351		1400
Sh1	(1340)	GTTGGGAGTCACTCAGTCTACCATCGCTCAAGCCTTGGAGAAAACCAAA		
Sus1	(1320)	CATGGCTGTACTCACTGTACCATTCCTCATGGCTTCAGAAAACCTAAGT		
Sus3	(1258)	GATGGCAATTACCCAGTCAACAATGCTCATGCTCTGCAAAAGACTAAGT		
Consensus	(1351)	GATGGGAGTTACTCAGTGTACCATTGCTCATGC CTGGAGAAAACCTAAGT		
		1401		1450
Sh1	(1390)	ACCCCAACTCGCAATCTACTTGGCAAAATTCGACAGCCAGTACCACTTC		
Sus1	(1370)	ACCGTAACCTCCAGCTCTACTGGAAGAGTTTGAGGATCACTACCACTTC		
Sus3	(1308)	ATGCAGATTACAGCATATTTTGAAGAATTTCATGAGAAGTACCATTC		
Consensus	(1401)	ACCC AACTC GACATCTACTGGAAGAA TTCGA GA CAGTACCACTTC		
		1451		1500
Sh1	(1440)	TCTTGGCAGTTCACAGCTCACCCTATTGGCATGAAACACACCGATTTCAT		
Sus1	(1420)	TGGTCCAGTTGACCACTGACTTGATTGCAATGAACCATGCCACTTCAT		
Sus3	(1358)	TCTTCCAGTTCACTGCTGATATAATTGGTATGAAACATGCTGATTTTAT		
Consensus	(1451)	TC TGCCAGTTCAC GCTGAC T ATTGC ATGAACCATGCCGATTTTCAT		
		1501		1550
Sh1	(1490)	CATCACCAGCACATTCCAAGAAATCGCGGAAGCAAGGACACCGTGGGGG		
Sus1	(1470)	CATCACCAGCTACTTCCAAGAGAGCGCCGAAACAAGGACACCGTCCGGCC		
Sus3	(1408)	CATCACCAGCACATCCAAGAAATTCCTGGAAGCAAAAATAGTGTTCGAC		
Consensus	(1501)	CATCACCAGCACATTCCAAGAAATCGC GGAAGCAAGGACACCGT GG C		
		1551		1600
Sh1	(1540)	AGTACGAGTCCCATATCCGGTCACTCTTCTGGGCTCTACCGTGTCTC		
Sus1	(1520)	AGTACGAGTCAACATGCGGTTCAAAATGCTGGCCTGTACCGCTTGTG		
Sus3	(1458)	AGTATGAGAGTCATACTGCTTTACTCTGCCTGGTCTGTACCGAGTTGTG		
Consensus	(1551)	AGTACGAGTC CATAT GCGTTCACTCTGCCTGG CTGTACCG GTGTGTC		
		1601		1650
Sh1	(1590)	CATGGCATCCATGTTTTCGATCCCAAGTTCAAGATTGCTCTCTCTGGAGC		
Sus1	(1570)	CACGGCATTCATGCTTCGACCCCAAGTTCAACATCGTGTCTCTGGCGC		
Sus3	(1508)	CATGGGATCCATGCTTCGATCCCAAGTTCAATATAGTCTCTCTCTGGAGC		
Consensus	(1601)	CATGGCATCGATGT TTCGATCCCAAGTTCAACAT GTCTCTCTCTGGAGC		

Figure 9c

1651 1700

Sh1 (1640) AGACATGAGTGTTTACTACCCCTTATACGGAAACCGACAAGAGACTCACCTG

Sus1 (1620) GGACCTGTGCATCTACTTCCCCATACCCGAGTCGCACAAGAGGCTGACCT

Sus3 (1558) TGACATGTCCATATACTTTCCACATAACGAGAAGGCCAAGCCACTCACCT

Consensus (1651) GACATGTCCAT TACTTCCC TATACCGAGACGGACAAGAGACTCACCT

1701 1750

Sh1 (1690) CCTTCATCCTGAAATCCAGGAGCTCATCTACAGCGACGTGAGAAATCC

Sus1 (1670) CCCTTCACCCGGAGATTGAGGAGCTCTGTACAGCCAAACCGAGAACAG

Sus3 (1608) CTCCTGATGGTTCAATCCGAAATTTGATTTATGACCGGAGCAAAACGAT

Consensus (1701) CCCTTCATCCTGAAATCGAGGAGCTCAT TACAGCCA G CGAGAAC C

1751 1800

Sh1 (1740) GAGCACAAGTTCGTGCTCAAGGACAAACAAGCCGATCATCTTCTCGAT

Sus1 (1720) GAGCACAAGTTCGTTCGACGACAGCAACAAGCCAATCATCTTCTCCAT

Sus3 (1658) CAACACATTGGGCATCTGGATGACCGGTCAAAGCCCATCTCTTCTCCAT

Consensus (1751) GAGCACAAGTTCGTTCGAA GACAGGAA AAGCC ATCATCTTCTCCAT

1801 1850

Sh1 (1790) GCGCGCTCTCGACCCCGTGAACAACATGACAGGCTTGGTCGAGATGTACG

Sus1 (1770) GCGTCGTCTCGACCGTGTGAACAACCTGACTGCGCTGCTGAGCTGTACG

Sus3 (1708) GCGAAGACTCGACAGGCTGAACAACATAACACGGCTGCTCGAAGCTTTTG

Consensus (1801) GGC CGTCTCGACCG GTGAAGAACATGACAGGCTGGTTCGAG TGTACG

1851 1900

Sh1 (1840) GCAAGAAGCGCGCTCAGGGAGCTGGCGAACCTCGTGATCGTTGCCGGT

Sus1 (1820) GCGCGAACAAGCGCTGCAGGAGCTGCTGAACCTCGTGCTCGTCTGCGGC

Sus3 (1758) CTAAGTGGCTAAGCTGAGGAGCTGGTAAGCTTGTCTGCTTGCCTGGG

Consensus (1851) GCAAGAAGCGCGCTGAGGGAGCTGGTGAACCTCGTGCTCGTTGCCGG

1901 1950

Sh1 (1890) GACCACGG --- CAAGGAGTCCAAGGACAGGGAGCAGCAGCGGAGTTCAA

Sus1 (1870) GACCATGG --- CAACCTTCCAAGGACAGGAGGAGCAGCGGAGTTCAA

Sus3 (1808) TCAATGATGTCAACAAGTCCAAGGACAGGGAAGCATCGCGGAGATAGA

Consensus (1901) GACCATGG CAAC AGTCCAAGGACAGGAGGAGCAGCGGAGTTCAA

1951 2000

Sh1 (1937) GAAGATGTACAGCCTCATCGACGAGTAGAACTTCAAGGCGCATATCCGCT

Sus1 (1917) GAAGATGTTTGACCTCATCGACGAGTAGAACCTCAACCGGGACATCCGCT

Sus3 (1858) GAAGATGCATGAACCTCATCAAGACCCACAACCTTGTTCGCGAGTTCCGCT

Consensus (1951) GAAGATGTATGACCTCATCGAG AGTACAACTTGAACGGGCA ATCCGCT

2001 2050

Sh1 (1987) GGATCTCTCGCGGAGATGAACCGTGTCCGCAACGGCGAGCTGTACCCTAC

Sus1 (1967) GGATCTCTCGCGGAGATGAACCGCGTCCGCAACGGCGAGCTGTACCCTAC

Sus3 (1908) GGATCTCTCGCGGAGCAAAACAGGGCCCTAACCCTGAGCTCTATCGCTAC

Consensus (2001) GGATCTC GCCAGATGAACCG GTCCGCAACGGCGAGCTGTACCCTAC

2051 2100

Sh1 (2037) ATTTCGATACCAAGGCGCATTCGTGCAGCCTGCGTTCTACGAAGCGTT

Sus1 (2017) ATCTGCCACACCAAGGCGCTTCGTGCAGCCTGCTTTCTACGAGGTTT

Sus3 (1958) ATCGCTGATACCATCTGCTTTCTGTACAGCGGCTTGTATGAAGCGTT

Consensus (2051) ATCTGCCATACCAAGGGCGC TTCGTGCAGCCTGC TTCTACGAAGCGTT

2101 2150

Sh1 (2087) CGGCCTGAGTGTGATCGAGTCCATGACGTGCGGTCTGCCAAGGATCGCGA

Sus1 (2067) CGGGCTGACCGGTGGTTCAAGCCATGACCTGCGGCTGCCCAAGGTCGCGA

Sus3 (2008) CGGTCTCACCGTCTGTTGAGCCATGACCTGTGGGCTTCCTACTTTCGCGA

Consensus (2101) CGG CTGAC GTGGTTGAGGCCATGACCTGCGG CTGCC ACGTTTCGCGA

2151 2200

Sh1 (2137) CCTGCCATCGCCGCCCTCTGAGATCATGCTGGACGGGGTATCTGGCTTG

Sus1 (2117) CCGCTTACCGCGGTTCGGCCGAGATCATGCTGCACGGCGTGTCTGGCTAC

Sus3 (2058) CGCTCCATCGAGGTCCAGCTGAGATCATAGCACTCGCGTCTCGGGCTTC

Consensus (2151) CC CCATGGCGGTCC GCTGAGATCATGCTGCACGGCGT TCTGGCTTC

Figure 9d

		2201	2250
Sh1	(2187)	CACATTGACCCTTACCACAGCCAGAACCCCGGGATATCCTGGTCAACTT	
Sus1	(2167)	CACATCGACCCTTACCAGGGGCGACAGCCGTCGGCCCTGCTCGTGCACTT	
Sus3	(2108)	CACATTGACCCTTACCAGCCCGAACAGGCTGTTAATCTGATGGCCGACTT	
Consensus	(2201)	CACATTGACCCTTACCAC GCGACAAGGC GCGGATCTGCTGGTCACTT	
		2251	2300
Sh1	(2237)	CTTTCACAAATGCAAGGCAGATCCGAGCTACTGGGACGAGATCTCACAGG	
Sus1	(2217)	CTTCGACAAGTGGCAGGCGGAGCCGAGCCACTGGAGCAAGATCTCCAGG	
Sus3	(2158)	CTTCGACCGGTGCAAGCAAGACCCAGATCACTGGTCAATATATCTGGAG	
Consensus	(2251)	CTTCGACAAGTGCAAGGCAGA CCGAGCCACTGGG CAAGATCTC CAGG	
		2301	2350
Sh1	(2287)	GCGGCCGTCAGAGAAATTTATGAGAAGTACACCTGCAAGCTCTACTCCGAG	
Sus1	(2267)	GCGGGCTCCAGCGTATCGAGGAGAAGTACACCTGCAAGCTGTACTCGGAG	
Sus3	(2208)	CAGGGCTGCAGGCGATATACGAGAAGTACACATGGAAGATATACTCAGAG	
Consensus	(2301)	GCGGGCTGCAGCG AT TA GAGAAGTACACCTGGAAGCT TACTC GAG	
		2351	2400
Sh1	(2337)	AGGCTGATGACCTTGACCGGCGGTCTACGGGTTCTGGAAGTACGTGAGCAA	
Sus1	(2317)	AGGCTGATGACCTTACCGGCGGTCTACCGGTTCTGGAAGTACGTGTCCAA	
Sus3	(2258)	AGGCTGATGACACTGGCCGGGCTCTACCGTTTCTGGAAGTACGTGTCCAA	
Consensus	(2351)	AGGCTGATGACCTTGACCGGCGGTCTACGGGTTCTGGAAGTACGTGTCCAA	
		2401	2450
Sh1	(2387)	CCTGGAGAGCGCGGAGACCCGCGCTACATCGAGATGTTCTACCGCGTGA	
Sus1	(2367)	CCTGGAGAGCGCGGAGACCCGCGCTACCTGGAGATGCTCTACCGCGTCA	
Sus3	(2308)	GCTCGAGAGCGCTGGAGAGGAGCGCTACCTTGAGATGTTCTACATACTGA	
Consensus	(2401)	CCTGGAGAGCGCGGAGACCCGCGCTACCT GAGATGTTCTACGC CTGA	
		2451	2500
Sh1	(2437)	AGTACCGTAGCCTGGCAAGCCAGGTTCCGCTGTCTCTCCA-----TTAG	
Sus1	(2417)	AGTACCGTAGCATGCGGAGCACCGTCCGCTCGGCGTCA-----GGGA	
Sus3	(2358)	AGTACCGTAGCTGGCGAAGACCGTCCGCTTGAATTCACCAACCCAG	
Consensus	(2451)	AGTACCGCA CCTGGCGAGCACCGTCCGCTGGCC T GA G AG	
		2501	2550
Sh1	(2481)	TACGGGGAAAGAACGAGA-AGAAGAACAGAAGCCAGGCCGA-----G	
Sus1	(2461)	GAGCCCTCCAGCAAGTGA-TCCGTGACGGCGGCCACAGACCTCATC---G	
Sus3	(2408)	TAGCTTGGCAACTGCCACTGCCGTAGCACTTGCTACAGACTGAACCTG	
Consensus	(2501)	TAGC GC AGAA G GA TGCCTAACA GGCACAGGCTGA G	
		2551	2600
Sh1	(2525)	AACCATCGCTGCATTTCCATCT-----GT-TTACCCGAATTCGC	
Sus1	(2507)	ATCGATGAGGAGAGGGAGCACTCGGA-----GT-GTGTGTCTTTTCC	
Sus3	(2458)	AAGACCTTCACTAATTTAGCGCGGCGAGACGCTAGCCAATAAAATGTGC	
Consensus	(2551)	AACGATC C G A TT G CTCGG GT GTCA CAATTGCG	
		2601	2650
Sh1	(2565)	ATTGTTAGTGTGTATTGGAGTTATGTG--TACTTGGTTTCCANGAAGTT	
Sus1	(2551)	TTGCCATTTCTTCTTCTTCTTTTCC--TTCCCGAGGGGCAAAAAAA	
Sus3	(2508)	CGGAGCTGAAGTCTTTTATTATGTACATAATGGCAGTATACAAAT	
Consensus	(2601)	TG TGTC TG TTT TT TTATGT TACT GGAGTC AA AAAAT	
		2651	2700
Sh1	(2613)	TGGTTCCTTCTCGTTTCTTCTTCTTCTGAGCTTTTGGGACGCGTG	
Sus1	(2599)	AGAGTC-TGCTT-TGCTAGGCGGCGGGCTTGGTTGCTGCTCTTTGCTT	
Sus3	(2558)	TACTGAAGGAGGTGGGTGTCAGTTGTGTCTTCTTACTG-----TT	
Consensus	(2651)	TG TTC TGCT GTTG TTG CGTTGTGTGTTCTGTT CTG C GCTT	
		2701	2750
Sh1	(2663)	GCTTCCTTCTAGTATGCTGGCAATGGCTGCACCTTTTGCTTCAATAA	
Sus1	(2647)	CAAGAGTTAAATTTACCTACC--TTGTCAAGGTCTTGTTCATCATTTGA	
Sus3	(2600)	TACTGTATTATGTCAAGCTGTG---GGGTGCAATTTCTTTGCTG--CA	
Consensus	(2701)	ACTGGTT ATATTAAGCTG C TTGGCTGCA CTT TTC TGA T A	

Figure 9e

```

                2751                                2800
Sh1 (2713) AAATGCCTGCTCGTTCACTGCTTCCAGAGTGC-----
Sus1 (2695) TCCGGGTGTGGCTTGTAGTACTCTGATGCACTGTACTAGTTTGGCGTTGC
Sus3 (2644) AGCCGCAGGGCACTGGTGAAGTGGTGATAAATACATCATATTCTGTTGACC
Consensus (2751) A C GC GGC CTTGTA GTCTGATAGA TG T TA T TG C
                2801                                2850
Sh1 (2747) -----
Sus1 (2745) GTCGGTTGACAGGGAAACGTTGGTGGTGGTGTGTGTGCAGTCAGGCGT
Sus3 (2694) TGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGCCGC-----
Consensus (2801) G A A AA G G G C

                2851                                2900
Sh1 (2747) -----
Sus1 (2795) GGTGCTCCCTTTGTTTCCTGGATGGGATGTTGCTCCTTGAATAATAATCG
Sus3 (2738) -----
Consensus (2851)

                2901                                2950
Sh1 (2747) -----
Sus1 (2845) TAGTGGCCTTGGAGCCCTTTTCCTGAAATAAGAGCAGCATCCTAGTGCTT
Sus3 (2738) -----
Consensus (2901)

                2951                                2964
Sh1 (2747) -----
Sus1 (2895) ACCTTTGCAGCTGT
Sus3 (2738) -----
Consensus (2951)

```

Figure 9f

CGCCAGTCGCCAGTCGCCACAGCCACACCACACCACACTAGCCGCGGCCGCGGGTAGGAG  
CGCGCGCGGCGCGGCGGAACGACCCACCGGTGGCGGCAGCCCATGTCTGCCCCGAAGCTGA  
ACCGCAACGCGAGCATCCGGGACCGCGTCGAGGACACCCTCCACGCGCACCGCAACGAGC  
TCGTCGCCCTCCTCTCCAAGTACGTGAACAAGGGGAAGGGCATCCTGCAGCCGCACCACA  
TCCTCGACGCGCTCGACGAGGTCCAGGGCTCCGGGGTCCGCGCGCTCGCCGAGGGACCCT  
TCCTCGACGTCCTCCGCTCCGCGCAGGAGGCGATCGTGCTGCCGCCG

**Figure 10**



**Sorghum sequence from SEQ ID NO: 13 in SEQ ID NO: 11**  
 ATGTCTGCCCGAAGCTGAACCGCAACGCGAGCATCCGG

**Maize sequence from SEQ ID NO: 1 in SEQ ID NO: 11**

gtcgaccac	gcctccggg	accgcgtcga	ggacaccctc	cacgcgcacc	gcaacgagct	60
cgctgccctc	ctgtccaagt	acgtgaacaa	ggggaagggc	atcctgcagc	cgcaccacat	120
cctcgacgcg	ctcgacgagg	tccagggctc	cgggggccc	gcgctagccg	agggaccctt	180
cctcgacgtc	ctccgctccg	cgcaggaggc	gatcgtgctg	ccgccgttcg	tggccatcgc	240
ggtgcgcccc	cgcccgggag	tttgggagta	cgcccgctc	aacgttcacg	agctcagcgt	300
cgagcagctc	acagtctcgg	agtacctcgg	cttcaaggag	gagcttgctg	acggccagca	360
caatgatccc	tacgtttctg	agcttgactt	cgagccgttc	aatgtctcag	tcccacgccc	420
aaatcgggtc	tcatctattg	gaaacggtgt	gcagttccct	aaccgacact	tgctcctcaat	480
catgtttccg	aacagggatt	gcttgaggcc	cctgttggtg	ttcctccgtg	gccaccggca	540
caaggggcat	gttatgatgc	ttaatgatag	aatacaaaag	ttggggaggc	ttcagttcgt	600
cctgaccaaa	gctgaggagc	acttggtcaaa	gctccctgct	gacacacccat	actcacaatt	660
tgcttataaa	tttcaagagt	ggggcctgga	gaaaggttgg	ggtgatacag	caggacatgt	720
tttggaaatg	atccatctcc	ttctagacat	cattcaggcg	ccagacccat	ctaccctaga	780
gaaattcttg	gggaggatcc	ccatgatttt	taacgtttgt	gtggtatccc	ctcatggata	840
ctttggtcaa	gctaattgat	taggcttgcc	agacacagga	ggacagatcg	tctatatact	900
ggaccaagtc	cgtgcactag	aaaatgagat	ggttctccgt	ttaaaagaaac	aagggttga	960
tgtttcccca	aagattctca	ttgttactcg	gctgatacca	gatgcaaaag	gaacatcatg	1020
caatcagcgg	cttgagagaa	ttagtggaa	acagcatact	tacataattac	gagttccctt	1080
cagaaatgaa	aatgggatac	ttaagaaatg	gatatacaaga	tttgatgtgt	ggccatatct	1140
ggaaacattt	gctgaggatg	ctgctgggtg	aattgctgct	gaattacaag	gtactccaga	1200
cttcataaatt	ggaaactaca	gtgatggaaa	tcttggtggc	tcattgctat	cttacaagat	1260
gggaattacc	cagtgcacaa	ttgctcatgc	tctggaaaag	actaagtatc	cagattcaga	1320
catatttttg	aagaatttcg	atgagaagta	ccatttctcc	tgccagttca	ctgctgatat	1380
aattgctatg	aacaatgctg	attttatcat	caccagcaca	taccaagaaa	ttgctggaag	1440
caaaaatact	gttgagcagt	atgagagtca	tactgccttt	actctgcctg	gtctgtaccg	1500
agttgtccat	gggatcgatg	tcttcgatcc	aaagtccaat	atagtctctc	ctggagctga	1560
catgtccata	tactttccac	ataccgagaa	ggccaagcga	ctcacctctc	ttcatggttc	1620
aatcgaaaat	ttgatattatg	acccgagca	aaacgatgaa	cacattgggc	atctggatga	1680
ccggtcaaag	cccatcctct	tctccatggc	aagactcgac	aggggtgaaga	acataacagg	1740
gctggtcgaa	gcttttgcta	agtgcgctaa	gctgagggag	ctggtaaacc	ttgtcgtcgt	1800
tgccgggtac	aatgatgtca	acaagtccaa	ggacagggaa	gagatcgccg	agatagagaa	1860
gatgcatgaa	ctcatcaaga	cccacaactt	gttcgggcag	ttccgctgga	tctctgccc	1920
gacaaacagg	gcccgtaacg	gcgagctcta	tcgctacatc	gctgatcccc	atggtgcttt	1980
cgtacagccg	gccttgatg	aagcgttcgg	tctcacccgtc	gttgaggcca	tgacctgtgg	2040
gcttctact	ttcgcgacgc	tccatggagg	tccagctgag	atcatagagc	atggcgtctc	2100
gggcttccac	attgacccgt	accaccccga	acaggctggt	aatctgatgg	ccgacttctt	2160
cgaccgggtc	aagcaagacc	cagatcactg	ggtgaatata	tctggagcag	ggctgcagcg	2220
catatacgag	aagtacacat	ggaagatata	ctcagagagg	ttgatgacac	tggccggggt	2280
ctacggtttc	tggaagtacg	tgtcgaagct	cgagaggctg	gagacgaggc	gctaccttga	2340
gatgtttctac	atactgaagt	tccgcgagct	ggcgaagacc	gtgccgcttg	caattgacca	2400
accgcagtag	cttcgcaac	tgcgactgcg	tagcacttgg	tacaagactg	aaacctgaag	2460
gaccttcagt	aatttaggcg	cggcagacgg	tagccaataa	aatgtgcccg	agctgaactg	2520
gttttttatt	atgtacataa	tggcagtata	acaaaattac	tgaaggcagg	tgggttgacg	2580
ttgtgtgttc	gttactgttt	actgtattat	gtcaagctgt	cggctgcaat	ttctttgctg	2640
gcaagccgca	ggcactggtg	aagtgcgtgat	aaatacatca	tattctgttg	acctgtgaaa	2700
aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	cgcccg			

**Figure 11**